Chapter 1

Object Oriented Programming

1.1 Object oriented approach

Definition 1.1.1: Object Oriented Programming

Object oriented programming (OOP) is a imperative programming programming paradigm where instructions are grouped together with the part of the state they operate on.

The main **structural components** of all systems are

- Objects: Object is something that takes up space in the real or conceptual world with which somebody may do things. An object is an instance of a class. An object has three main characteristics:
  - Name (or ID): Unique identifier for the object.
  - State: Attributes that describe the object.
  - Operations (or behavior): Actions that the object can perform.
- Class objects: Class is the blueprint of an object.

Main **characteristics** of the approach are

- Encapsulation: The mechanism of hiding the implementation of the object. Only the necessary details are exposed to the user.
- Abstraction: A principle which consists of ignoring the aspects of a subject that is not relevant for the present purpose. It is the process of simplifying complex systems by modeling classes based on the essential properties and behaviors an object must have.
- Inheritance: Mechanism by which one class can inherit attributes and methods from another class. Making new classes from existing ones.
- Polymorphism: Ability to present the same interface for different data types. Same function name but different signatures being used for different types.

1.2 Class

Definition 1.2.1: Class Diagram

A class diagram is a type of static structure diagram that describes the structure of a system by showing the system's classes, their attributes, operations (or methods), and the relationships among objects.

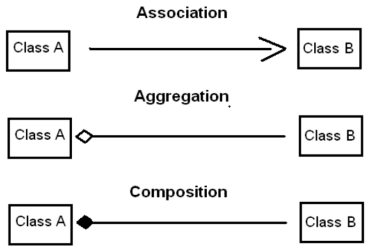
Elements of a **class**:

- Class Name (ID Class): The name of the class. Nouns associated with the textual description of a problem. Singular.

- Attributes: The properties or characteristics of the class. Types include Real, Integer, Text, Boolean, Enumerated, etc.
- Operations (Methods): The functions or operations that can be performed on the class. Behaviors of the class.

Relations between classes:

- Association: A relationship between two classes that indicates how objects of one class are connected to objects of another class.
- Aggregation: A special type of association that represents a "whole-part" relationship between classes.
- Composition: A stronger form of aggregation that implies ownership and a whole-part relationship where the part cannot exist independently of the whole.
- Generalization: A relationship between a more general class (superclass) and a more specific class (subclass) that indicates inheritance.



1.2.1 Class and Method in Python

```python
class Person:
    pass # An empty class definition

p = Person()
print(p)  # Output: <__main__.Person object at 0x...>
```

Listing 1.1: Empty class definition in Python

```python
"""Define class with method"""
class Person:
    def speak(self):
        print("Hello!")

"""Create object and call method"""
p = Person()
p.speak()  # Output: Hello!
```

Listing 1.2: Method

```python
"""
The __init__ method is a special method in Python classes.
It is a method that Python calls when you create a new instance of this class.
"""
class Person:
    def __init__(self, name):
        self.name = name  # Initialize the name attribute
    def speak(self):
        print('Hello, my name is', self.name)

p = Person('Carlos')
p.speak()  # Output: Hello, my name is Carlos
```

Listing 1.3: Attributes and __init__ method

Note:

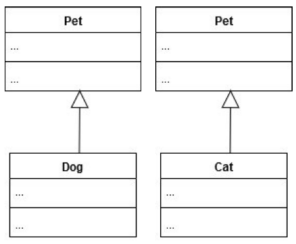
The first argument of every class method, including init, is always a reference to the current instance of the class. By convention, this argument is always named self.

```
class Pet(object):
    def __init__(self, name, species):
        self.name = name
        self.species = species
    def getName(self):
        return self.name
    def getSpecies(self):
        return self.species
    def __str__(self):
        return "%s is a %s" % (self.name, self.species)
```

Listing 1.4: Class Pet with attributes and methods

```
class Dog(Pet):

"""Dog inherits from Pet"""

    def __init__(self, name, chases_cats):
        # Call the parent class (Pet) constructor
        Pet.__init__(self, name, "Dog")
        self.chases_cats = chases_cats

    def chasesCats(self):
        return self.chases_cats

class Cat(Pet):

"""Cat inherits from Pet"""

    def __init__(self, name, hates_dogs):
        # Call the parent class (Pet) constructor
        Pet.__init__(self, name, "Cat")
        self.hates_dogs = hates_dogs

    def hatesDogs(self):
        return self.hates_dogs
```

Listing 1.5: Inheritance



Example 1.2.1 (Inheritance)

myPet = Pet("Boby", "Dog")
myDog = Dog("Rex", True)

- isinstance(myDog, Pet) # Returns: True
- isinstance(myDog, Dog) # Returns: True

- isinstance(myPet, Pet) # Returns: True
- isinstance(myPet, Dog) # Returns: False

1.2.2 Access Modifiers

There are three types of access modifiers in Python:

- Public: Members (attributes and methods) declared as public are accessible from anywhere.
- Protected: Members declared as protected are accessible within the class and its subclasses. In Python, this is indicated by a single underscore prefix (e.g., _attribute).
- Private: Members declared as private are accessible only within the class itself. In Python, this is indicated by a double underscore prefix (e.g., __attribute).

```
class Person:
    def __init__(self, name, age):
        self.__name = name      # Private attribute
        self.__age = age        # Private attribute

p = Person("David", 23)
p.__name  # This will raise an AttributeError
```

Listing 1.6: Private Attributes

```
class Person:
    def __init__(self, name, age):
        self.name = name      # Public attribute
        self.age = age        # Public attribute

p = Person("David", 23)
p.name  # This will work fine and return "David"
```

Listing 1.7: Public Attributes

```
class Person:
    def __init__(self, name, age):
        self._name = name      # Protected attribute
        self._age = age        # Protected attribute

p = Person("David", 23)
p._name  # This will work, but it's discouraged to access protected members directly
```

Listing 1.8: Protected Attributes

```
class Person:
    def __init__(self, money=0, energy=100):
        self.money = money
        self.energy = energy

    def work(self, hours):
        if self.energy >= hours * 10:
            self.money += hours * 10 # Assume earning $10 per hour of work
            self.energy -= hours * 10
            print (f"Worked for {hours} hours. Money increased to ${self.money}, energy
                decreased to {self.energy}.")
        else:
            print("Not enough energy to work.")
```

Listing 1.9: Example Usage

Chapter 2

Data Analysis and Statistics

2.1 Numpy

Definition 2.1.1: Numpy

Numpy is a fundamental package for scientific computing in Python. It provides support for arrays, matrices, and many mathematical functions to operate on these data structures efficiently.

2.1.1 Shape, rank, and size

```
    c = np.array([1, 2, 3, 4])  # Create a 1D array
    print(type(c))  # Output: <class 'numpy.ndarray'>

    b = np.array([[1, 2, 3], [4, 5, 6]])  # Create a 2D array
    shape = b.shape  # Output: 2, 3
    rank = np.ndim(b)  # Output: 2
    size = b.size  # Output: 6
```

Listing 2.1: Shape, rank, and size

2.1.2 Maniputating arrays

Reshaping arrays means changing the shape of an array. The shape of an array is the number of elements in each dimension. By reshaping, we can add or remove dimensions or change number of elements in each dimension.

```
    arr = np.array([4, 4, 3, 4, 5, 6, 7, 9, 0, 10, 17, 12])
    newarr = arr.reshape(3, 4)  # Reshape to 3 rows and 4 columns
    print(newarr)
    # Output:
    # [[ 4  4  3  4]
    #  [ 5  6  7  9]
    #  [ 0 10 17 12]]
```

Listing 2.2: Reshaping an array

We can also access an array element and change value to an array.

```
    a = np.array([10, 20, 30, 40, 50])
    a[2] = 50  # Change the third element to 50
    print(a)  # Output: [10 20 50 40 50]
```

Listing 2.3: Accessing and changing array elements

```
a = np.zeros((2,2))  # Create a 2x2 array of zeros
b = np.ones((3,3))   # Create a 3x3 array of ones
c = np.full((2,3), 7)  # Create a 2x3 array filled with 7s
d = np.eye(3)    # Create a 3x3 identity matrix
```

Listing 2.4: Creating special arrays

Joining NumPy arrays means putting contents of two or more arrays into a single array.

```
a = np.array([1, 2, 3])
b = np.array([4, 5, 6])

c = np.concatenate((a, b))  # Join a and b
print(c)  # Output: [1 2 3 4 5 6]

d = np.stack((a, b), axis=0)  # Stack a and b vertically
print(d)
# Output:
# [[1 2 3]
#  [4 5 6]]

e = np.stack((a, b), axis=1)  # Stack a and b horizontally
print(e)
# Output:
# [[1 4]
#  [2 5]
#  [3 6]]
```

Listing 2.5: Joining NumPy arrays

```
a = np.array([[1,2,3,4], [5,6,7,8], [9,10,11,12]])
print(a)
# Output:
# [[ 1  2  3  4]
#  [ 5  6  7  8]
#  [ 9 10 11 12]]

b = a[:3, 1:3]  # Slicing rows 0-2 and columns 1-2
print(b)
# Output:
# [[ 2  3]
#  [ 6  7]
#  [10 11]]
```

Listing 2.6: Slicing NumPy arrays

Problem 2.1: Slicing arrays

b[0, 0] = 20
What happens to array a?
Answer: Array a is also changed because b is a view of a.

Problem 2.2: Slicing arrays

How to get a copy of a slice of an array so that changes to the slice do not affect the original array?
Answer: Use the .copy() method to create a copy of the slice.

```
b = a[:3, 1:3].copy()  # Create a copy of the slice
b[0, 0] = 20  # Change the first element of b
```

```
print(a)  # Array a remains unchanged
# Output:
# [[ 1  2  3  4]
#  [ 5  6  7  8]
#  [ 9 10 11 12]]
```

Listing 2.7: Creating a copy of a slice

2.1.3 Handling indexes

```
a = np.array([[1, 2, 3], [4, 5, 6], [7, 8, 9], [10, 11, 12]])
print(a)
# Output:
# [[ 1  2  3]
#  [ 4  5  6]
#  [ 7  8  9]
#  [10 11 12]]

b = np.array([0, 2, 0, 1])
print(a[np.arange(4), b])  # Access elements using array of indices
# Output: [ 1  6  7 11]

a[np.arange(4), b] += 10  # Increment selected elements by 10
print(a)
# Output:
# [[11  2  3]
#  [ 4  5 16]
#  [17  8  9]
#  [10 21 12]]
```

Listing 2.8: Fancy indexing

```
b = 1
b += 10
print(b)  # Output: 11

b = 1
b = b+10
print(b)  # Output: 11
```

Listing 2.9: Boolean indexing

```
grades = np.array([14, 12, 13, 14, 15, 14, 14])
x = np.where(grades == 14)  # Find indices where grades are 14
print(x)  # Output: (array([0, 3, 5, 6]),)
```

Listing 2.10: Searching arrays

2.1.4 Random

Definition 2.1.2: Random

Random number does not mean a different number each time. Random means something that cannot be predicted logically.

```
from numpy import random

# Generating random numbers within an array
e = np.random.random((4, 4)) # Create a 4x4 array of random floats in [0.0, 1.0)
```

```
    # Generating random numbers
    x = random.randint(100)  # Generate a random integer from 0 to 99

    # Generating arrays of random numbers
    x = random.randint(100, size=(5)) # Generate an array of 5 random integers from 0 to 99
    x = random.randint(100, size=(3, 4)) # Generate a 3x4 array of random integers from 0
        to 99
    x = random.rand(5)  # Generate an array of 5 random floats in [0.0, 1.0)
```

Listing 2.11: Generating random numbers

Definition 2.1.3: Random data distribution

A random distribution is a set of random numbers that follow a certain probability density function (PDF).

- Normal distribution (random.normal)
  - loc: (mean) where the peak of the bell curve is located
  - scale: (standard deviation) how flat and wide the bell curve is
  - size: output shape
- Binomial distribution (random.binomial)
  - n: number of trials
  - p: probability of success on each trial
  - size: output shape

```
    # Normal Distribution
    x = random.normal(loc=0.0, scale=1.0, size=(2,3))  # Generate a 2x3 array of random
        numbers from a normal distribution
    print(x)
    # Output:
    # [[ 0.49671415 -0.1382643   0.64768854]
    #  [ 1.52302986 -0.23415337 -0.23413696]]

    # Binomial Distribution
    x = random.binomial(n=10, p=0.5, size=(3,4))  # Generate a 3x4 array of random numbers
        from a binomial distribution
    print(x)
    # Output:
    # [[5 6 4 3]
    #  [4 7 6 4]
    #  [6 3 5 4]]
```

Listing 2.12: Generating random numbers from different distributions

2.2 Pandas

Definition 2.2.1: DataFrame

Labelled data structure with columns of potentially different types. Like a spreadsheet or SQL table, or a dict of Series objects.

```
    d = {
        'col1': [1,2,1,3,1,2],
        'col2': [1,2,3,4,5,6]
        }
    df = pd.DataFrame(data=d)

    df.count() # Count non-NA cells for each column
    df['col1'].value_counts() # Count unique values in col1
    df['col1'][1] = 5 # Change value in col1 at index 1 to 5
```

Listing 2.13: Creating and manipulating a DataFrame

Problem 2.3: Copy DataFrames

col1 = df['col1'] # Accessing a single column
col1[2] = 99
What is the result in col1 and df?
Answer: Both col1 and df are changed because col1 is a view of df.

Problem 2.4: Copy DataFrames

new_col1 = col1.copy()
new_col[2] = 9999

What is the result in new_col1 and df?
Answer: Only new_col1 is changed, df remains unchanged because new_col1 is a copy of col1.

```
    df = pd.read_csv('data.csv')  # Read data from a CSV file into a DataFrame
    df.to_csv('output.csv')  # Write DataFrame to a CSV file
```

Listing 2.14: Read and save

```
    df.head()  # Display the first 5 rows of the DataFrames
    df.info()  # Display a summary of the DataFrame
    df.describe()  # Generate descriptive statistics
    df.columns  # List all column names
```

Listing 2.15: DataFrame information

```
    df.at(2, 'col1')  # Access a single value for a row/column label pair
    df.iloc[2, 0]  # Access a single value for a row/column pair by integer position
    df.xs(2)  # Returns cross-section (row) at index 2
    df.loc[:, 'col1']  # Access a group of rows and columns by labels or a boolean array
```

Listing 2.16: Accessing DataFrame elements

Example 2.2.1 (Access to row and columns)

- Cells: df.iloc[195][0]
- Rows: df.iloc[[195], :]
- Columns: df.loc[:, 'col1']

```
    df1=df2 # Assignment
    copydf = df.copy(deep=False) # Shallow copy
    copydf = df.copy(deep=True)  # Deep copy
```

Listing 2.17: Copying DataFrames

```
    # Convert column to numeric, setting errors to NaN
    df['GDP'] = pd.to_numeric(df['GDP'], errors='coerce')

    # Suppose you have , instead of . in the numbers
    df['GDP'] = df['GDP'].str.replace(',', '.')

    # Suppose you have $ or € symbols in the numbers
    df['GDP'] = df['GDP'].str.replace('$', '', regex=True).str.replace('€', '', regex=True)

    # Drop rows with any NaN values
    df.dropna(inplace=True)
```

Listing 2.18: Data cleaning and conversion

```
    X.mean()  # Calculate mean of each column
    X.median()  # Calculate median of each column
    X.mode()  # Calculate mode of each column
    X.std()  # Calculate standard deviation of each column
    X.var()  # Calculate variance of each column
    X.corr()  # Calculate correlation matrix
    X.cov()  # Calculate covariance matrix
    X.max()  # Calculate maximum of each column
    X.min()  # Calculate minimum of each column
    X.kurt()  # Calculate kurtosis of each column
    X.skew()  # Calculate skewness of each column
```

Listing 2.19: Statistical methods

2.3 Statistics

2.3.1 Statistics module

For averages and measures of central location, we have the following functions in the statistics module:

- mean(): Calculate the arithmetic mean of a list of numbers.
- harmonic_mean(): Calculate the harmonic mean of a list of numbers.
- median(): Calculate the median (middle value) of a list of numbers.
- median_low(): Calculate the low median of a list of numbers.
- median_high(): Calculate the high median of a list of numbers.
- mode(): Calculate the mode (most common value) of a list of numbers.
- stdev(): Calculate the standard deviation of a list of numbers.
- variance(): Calculate the variance of a list of numbers.
- pstdev(): Calculate the population standard deviation of a list of numbers.
- pvariance(): Calculate the population variance of a list of numbers.

There are also other packages that could be used, such as NumPy,Pandas, and SciPy, which provide more advanced statistical functions and methods for data analysis.

2.3.2 Statistical tests

```
improt numpy as np
import matplotlib.pyplot as plt

mu, sigma = 0, 0.1  # mean and standard deviation
a = np.random.normal(mu, sigma, 1000)  # Generate 1000 random numbers from a normal
    distribution
```

Listing 2.20: Generating random numbers from a normal distribution

```
from scipy import stat

stat, p = stats.normaltest(a)  # Perform D'Agostino and Pearson's test for normality

if p < 0.05:
    print("The data is not normally distributed")
else:
    print("The data is normally distributed")

stat, p = stats.shapiro(a)  # Perform Shapiro-Wilk test for normality

if p < 0.05:
    print("The data is not normally distributed")
else:
    print("The data is normally distributed")
```

Listing 2.21: Normality tests

Definition 2.3.1: Student's t-test

This is a two-sided test for the null hypotehsis that 2 independent samples have identical average (expected) values.

```
from scipy import stats

# Generate two independent samples
group1 = np.random.normal(loc=0, scale=1, size=100)  # Sample from group 1
group2 = np.random.normal(loc=0.5, scale=1, size=100)  # Sample from group 2

# Perform the t-test
stat, p = stats.ttest_ind(group1, group2, equal_var=False)  # Use Welch's t-test for
    unequal variances

if p < 0.05:
    print("The means of the two groups are significantly different")
else:
    print("The means of the two groups are not significantly different")
```

Listing 2.22: Student's t-test

Definition 2.3.2: Paired student's t-test

This is a two-sided test for the null hypothesis that 2 related or repeated samples have identical average (expected) values.

```
from scipy import stats

# Generate two related samples
before = np.random.normal(loc=0, scale=1, size=100)  # Sample before treatment
```

```
    after = before + np.random.normal(loc=0.5, scale=1, size=100)  # Sample after treatment
        (related to before)

    # Perform the paired t-test
    stat, p = stats.ttest_rel(before, after)

    if p < 0.05:
        print("The means of the two related groups are significantly different")
    else:
        print("The means of the two related groups are not significantly different")
```

Listing 2.23: Paired Student's t-test

Definition 2.3.3: Analysis of Variance Test (ANOVA)

The one-way ANOVA tests the null hypothesis that two or more groups have the same population mean. It is an extension of the t-test for more than two groups, possibly with different sample sizes.

```
    from scipy import stats

    # Generate three independent samples
    group1 = np.random.normal(loc=0, scale=1, size=100)  # Sample from group 1
    group2 = np.random.normal(loc=0.5, scale=1, size=100)  # Sample from group 2
    group3 = np.random.normal(loc=1, scale=1, size=100)  # Sample from group 3

    # Perform the one-way ANOVA test
    stat, p = stats.f_oneway(group1, group2, group3)

    if p < 0.05:
        print("At least one group mean is significantly different from the others")
    else:
        print("All group means are not significantly different from each other")
```

Listing 2.24: ANOVA

2.4 Time Series

The purpose of time series analysis is to understand the underlying structure and function that produced the observed data, and to fit a model and make forecasts.

To decompose time series data, we can use the seasonal_decompose function from the statsmodels library, which decomposes a time series into its trend, seasonal, and residual components.

We can also plot the autocorrelation function (ACF) and partial autocorrelation function (PACF) to identify the presence of autocorrelation in the data, which can help us determine the appropriate order of an ARIMA model for forecasting.

The ARIMA (AutoRegressive Integrated Moving Average) model is a popular method for forecasting time series data, which combines autoregressive (AR) and moving average (MA) components, along with differencing to make the data stationary.

After fitting the model, we can check the residuals to ensure that they are normally distributed and do not exhibit autocorrelation, which would indicate that the model is a good fit for the data.

We can also train and test the data by splitting the time series into a training set and a test set, fitting the model on the training data, and evaluating its performance on the test data using metrics such as mean absolute error (MAE) or root mean squared error (RMSE).

```
    import statsmodels.tsa.api as tsa
    import pandas as pd
    import matplotlib.pyplot as plt
    from pandas.plotting import autocorrelation_plot
    import statsmodels.tsa.api as tsa
```

```
    from math import sqrt
    from sklearn.metrics import mean_squared_error

    # Load time series data
    df = pd.read_csv('tourismPortugal.csv', sep=';')
    df['month'] = pd.to_datetime(df['month'])
    df = df.set_index(df['month'])
    df = df.drop(['month'], axis=1)

    # Decompose the time series into trend, seasonal, and residual components
    result = tsa.seasonal_decompose(df, model='multiplicative', period=12)

    figure = result.plot() # Plot the decomposed components

    # Plot the autocorrelation function (ACF) and partial autocorrelation function (PACF)
    serie = df[['tourists', 'month']]
    autocorrelation_plot(serie) # Plot the ACF
    plt.show()

    # Fit an ARIMA model to the data
    serie = serie.set_index('month')
    serie.index = series.index.to_period('M') # Convert index to monthly periods

    p = 4 # Order of the autoregressive part
    d = 1 # Degree of differencing
    q = 0 # Order of the moving average part

    model = tsa.arima.ARIMA(serie, order=(p, d, q))
    results = model.fit()
    print(results.summary()) # Print the model summary

    # Check the residuals
    residuals = pd.DataFrame(results.resid)
    residuals.plot(title="Residuals") # Plot the residuals
    plt.show()

    residuals.plot(kind='kde', title='Density of Residuals') # Plot the density of
        residuals
    plt.show()

    print(residuals.describe()) # Print the summary statistics of residuals

    # Train and test the model
    X = serie.values
    size = int(len(X) * 0.70) # Split the data into training and test sets
    train, test = X[0:size], X[size:len(X)]
    hisotry = [x for x in train]
    predictions = list()

    # Walk-forward validation
    for t in range(len(test)):
        model = tsa.arima.ARIMA(history, order=(p, d, q))
        model_fit = model.fit()
        output = model_fit.forecast()
        yhat = output[0]
        predictions.append(yhat)
        obs = test[t]
        history.append(obs)
        print('predicted=%f, expected=%f' % (yhat, obs))

    # Evaluate forecasts
```

```
    rmse = sqrt(mean_squared_error(test, predictions))
    print("Test RMSE: %.3f", rmse)

    # Plot the actual vs predicted values
    plt.plot(test)
    plt.plot(predictions, color='red')
    plt.show()
```

Listing 2.25: Time series analysis and forecasting

Other approaches such as LSTM, Prophet, and GARCH models can also be used for time series forecasting, especially when dealing with non-linear patterns or volatility in the data.

2.5 Regression

The main statsmodels API is split into models:

- statsmodels.api: The main API for statistical models, including linear regression, generalized linear models, and time series analysis. Cross-sectional models and methods.
- statsmodels.formula.api: Provides a formula interface for specifying statistical models using R-style formulas. A convenience interface for specifying models using formula strings and DataFrames.
- statsmodels.tsa.api: Contains tools for time series analysis, including ARIMA models, seasonal decomposition, and forecasting. Time-series models and methods.
- statsmodels.graphics.api: Provides functions for visualizing statistical models and results, such as residual plots and influence plots.

2.5.1 Linear regression

Linear models with independently and identically distributed errors, and for errors with heteroscedasticity or autocorrelation of unknown form.

- OLS (Ordinary Least Squares): A linear regression model that estimates the relationship between a dependent variable and one or more independent variables by minimizing the sum of squared residuals. Assumptions: linearity, independence, homoscedasticity, normality of errors, and no multicollinearity.
- GLM (Generalized Linear Models): A flexible generalization of linear regression that allows for response variables that have error distribution models other than a normal distribution. It includes logistic regression, Poisson regression, and others. Assumptions: the response variable follows an exponential family distribution, the link function is correctly specified, and the observations are independent.
- GEE (Generalized Estimating Equations): A method for estimating the parameters of a generalized linear model with possible correlation between outcomes. It is used for longitudinal data analysis and clustered data. Assumptions: the correlation structure of the data is correctly specified, and the observations are independent across clusters. Instead of assuming independent observations, GEE accounts for within-subject correlation.
- GAM (Generalized Additive Models): A generalization of linear models that allows for non-linear relationships between the dependent and independent variables by using smooth functions. It is used for modeling complex relationships in data. Assumptions: the response variable follows an exponential family distribution, the link function is correctly specified, and the observations are independent. GAMs do not assume a specific functional form for the relationship between the dependent and independent variables, allowing for more flexibility in modeling non-linear relationships.
- Robust linear models: These models are designed to be less sensitive to outliers and violations of assumptions than traditional linear regression models. They include methods such as Huber regression and RANSAC (Random Sample Consensus). Assumptions: Robust linear models do not rely on the same assumptions as traditional linear regression models, such as normality of errors or homoscedasticity. Instead, they are designed to be more flexible and robust to violations of these assumptions, making them suitable for data with outliers or non-normal error distributions.

- LMM (Linear Mixed Models): These models are used for data that have both fixed effects (parameters associated with an entire population) and random effects (parameters associated with individual experimental units). They are commonly used in fields such as psychology, ecology, and medicine for analyzing data with hierarchical or nested structures. Assumptions: linearity, normality of residuals, homoscedasticity, and independence of observations. Additionally, LMMs assume that the random effects are normally distributed and that the fixed effects are correctly specified. LMMs are particularly useful for analyzing data with repeated measures or clustered data, where observations are not independent, as they can account for the correlation between observations within clusters or subjects.

2.5.2 OLS assumptions

OLS assumes a **linear relationship** between the independent variables and the dependent variable. Verification methods include scatter plots to visualize the relationship between independent variables and the dependent variable. Residual plots by plotting the residuals against the fitted values to check for patterns that indicate non-linearity. And polynomial features by fitting a polynomial regression to see if higher-order terms improve the model fit.

```
import numpy as np
import pandas as pd
import statsmodels.api as sm
import matplotlib.pyplot as plt
import seaborn as sns

# Example dataset
df = pd.DataFrame({
    'X': np.linspace(1, 100, 100),
    'Y': np.linspace(1, 100, 100) + np.random.normal(0, 5, 100)
})

# Fit OLS model
X = sm.add_constant(df['X']) # Add intercept
model = sm.OLS(df['Y'], X).fit()

# Scatter plot
sns.regplot(x=df['X'], y=df['Y'],
scatter_kws={'alpha':0.5},
line_kws={"color":"red"})
plt.title("Checking Linearity with Scatter Plot")
plt.show()

# Residual plot
plt.scatter(
    model.fittedvalues, model.resid, alpha=0.5)
plt.axhline(y=0, color='red', linestyle='--')
plt.xlabel("Fitted Values")
plt.ylabel("Residuals")
plt.title("Residual Plot for Linearity Check")
plt.show()
```

Listing 2.26: Checking linearity assumption in OLS

Multicollinearity occurs when two or more independent variables in a regression model are highly correlated, meaning that one can be linearly predicted from the others with a substantial degree of accuracy. This can lead to unstable estimates of regression coefficients and make it difficult to determine the individual effect of each independent variable on the dependent variable. Verification methods include correlation matrix by calculating the correlation coefficients between independent variables to identify pairs that are highly correlated. Variance Inflation Factor (VIF) by calculating the VIF for each independent variable, where a VIF value greater than 5 or 10 indicates a potential multicollinearity problem.

```
from statsmodels.stats.outliers_influence import variance_inflation_factor

# Create feature matrix
X = pd.DataFrame({'X1': np.random.rand(100), 'X2': np.random.rand(100) * 2,
```

```
        'X3': np.random.rand(100) * 3})
    X = sm.add_constant(X)

    # Compute VIF for each variable
    vif_values = []
    for i in range(X.shape[1]):
        vif = variance_inflation_factor(X.values, i)
        vif_values.append((X.columns[i], vif))

    # Convert to DataFrame
    vif_data = pd.DataFrame(vif_values, columns=["Variable", "VIF"])
    # Display the results
    print(vif_data)
```

Listing 2.27: Checking multicollinearity using VIF

Residuals should have constant variance, **homoscedasticity**, across all levels of the independent variables. Verification methods include residual plots by plotting the residuals against the fitted values to check for patterns that indicate heteroscedasticity. Breusch-Pagan test by performing the Breusch-Pagan test to statistically assess the presence of heteroscedasticity, where a significant p-value indicates heteroscedasticity.

```
    import statsmodels.stats.diagnostic as smd

    # Residual plot
    plt.scatter(model.fittedvalues, model.resid, alpha=0.5)
    plt.axhline(y=0, color='red', linestyle='--')
    plt.xlabel("Fitted Values")
    plt.ylabel("Residuals")
    plt.title("Checking Homoscedasticity")
    plt.show()

    # Breusch-Pagan Test
    bp_test = smd.het_breuschpagan(model.resid,
        model.model.exog)
    print(f"Breusch-Pagan p-value: {bp_test[1]}")
```

Listing 2.28: Checking homoscedasticity

The residuals should not be correlated. This is important in time series data, where autocorrelation can be a common issue. Verification methods include autocorrelation function (ACF) plot by plotting the ACF of the residuals to check for significant autocorrelation at different lags. Durbin-Watson test by performing the Durbin-Watson test to statistically assess the presence of autocorrelation, where a value close to 2 indicates no autocorrelation, values less than 2 indicate positive autocorrelation, and values greater than 2 indicate negative autocorrelation.

```
    from statsmodels.stats.stattools import durbin_Watson

    dw_stat = durbin_watson(model.resid)
    print(f"Durbin-Watson Statistic: {dw_stat}")
```

Listing 2.29: Checking autocorrelation of residuals

The residuals should be approximately normally distributed, which is important for the validity of hypothesis tests and confidence intervals in OLS regression. Verification methods include Q-Q plot by creating a Q-Q plot of the residuals to visually assess their normality, where points should approximately follow a straight line if the residuals are normally distributed. Shapiro-Wilk test by performing the Shapiro-Wilk test to statistically assess the normality of the residuals, where a significant p-value indicates that the residuals are not normally distributed. Histogram and KDE plot by plotting a histogram and kernel density estimate (KDE) of the residuals to visually assess their distribution, where a bell-shaped curve suggests normality.

```
    import scipy.stats as stats

    # Histogram and KDE
    sns.histplot(model.resid, kde=True, bins=30)
```

```
    plt.title("Residuals Distribution")
    plt.show()

    # Q-Q Plot
    sm.qqplot(model.resid, line="45")
    plt.title("Q-Q Plot for Residuals")
    plt.show()

    # Shapiro-Wilk Test
    shapiro_test = stats.shapiro(model.resid)
    print(f"Shapiro-Wilk p-value: {shapiro_test.pvalue}")
```

Listing 2.30: Checking normality of residuals

Note:

The summary() function in Statsmodels provide important regression output, but it does not directly test OLS assumptions. However, it gives useful clues about potential violation.

- R-squared and adjusted R-squared: indicate model fit but do not test assumptions.
- F-statistics and Prob (F-statistics): tests if at least one predictor is significant.
- Coefficients and p-values: show predictor significance but do not check multicollinearity.
- Standard errors: can be affected by heteroskedasticity.
- Durbin-Watson statistic: helps detect autocorrelation, should be close to 2.
- Omnibus and Jacque-Bera tests: check for normality of residuals, should have a high p-value.

```
    import statsmodels.api as sm

    model = sm.OLS(y,X).fit()
    print(model.summary())
```

Listing 2.31: Fitting an OLS model and checking assumptions

Chapter 3

Data Visualization

3.1 Matplotlib

Matplotlib is a powerful and versatile Python library for creating static. It supports different chart types including scatter plots, line charts, and bar charts. While highly flexible, it can sometimes feel verbose for simple visualizations. It serves as the backbone for other libraries like Seaborn and Plotly, which build on its capabilities to provide more user-friendly interfaces for specific types of visualizations.

Strengths:

- Control over plot elements
- Wide range of plot types
- Suitable for publication-quality figures

Weaknesses:

- Can be verbose for simple plots
- Steeper learning curve for beginners

The building blocks of Matplotlib include:

- **Figure**: The overall container for the plot. Includes one or more subplots. It is like a blank canvas where multiple charts can be arranged.
- **Axes**: The area where the data is plotted, which can contain multiple subplots each displaying a different visualization.
- **Subplot**: A specific area within the figure where a plot is drawn, allowing for multiple plots in one figure. Useful for comparing different datasets side by side.
- **Axis**: Corresponds to the x and y axes of a plot, which can be customized with labels, ticks, and limits to enhance readability and presentation.

```
1  import matplotlib.pyplot as plt
2
3  # Figure
4
5  fig = plt.figure(figsize=(8, 6)) # creates a new figure with a specified size of 8
       inches by 6 inches. This figure serves as the canvas for plotting.
6  ax = fig.add_subplot(111) # adds a single subplot to the figure. The '111' argument
       indicates that the subplot should occupy the entire figure (1 row, 1 column, 1st
       subplot).
7  plt.show() # displays the figure with the subplot. Since no data has been plotted yet,
       it will show an empty plot.
8
```

```
    # Axes
    fig, ax = plt.subplots() # creates a new figure and a single set of axes (subplot) in one step. This is a more concise way to create a figure and axes compared to the previous method.
    ax.plot([1, 2, 3], [4, 5, 6]) # plots a line graph on the axes using the provided x and y data points. The x values are [1, 2, 3] and the corresponding y values are [4, 5, 6].
    plt.show() # displays the figure with the plotted line graph.

    # Subplots
    fig, (ax1, ax2) = plt.subplots(1, 2) # creates a new figure with two subplots arranged in one row and two columns. The variables ax1 and ax2 refer to the first and second subplot, respectively.
    ax1.plot([1, 2, 3], [4, 5, 6], label="Dataset 1") # plots a line graph on the first subplot (ax1) using the provided x and y data points.
    ax2.scatter([1, 2, 3], [4, 5, 6], color="r", label="Dataset 2") # plots a scatter graph on the second subplot (ax2) using the same x and y data points.
    plt.show() # displays the figure with both subplots: the first showing a line graph and the second showing a scatter graph.

    # Axis
    fig, ax = plt.subplots() # creates a new figure and a single set of axes (subplot) in one step.
    ax.plot([1, 2, 3], [4, 5, 6]) # plots a line graph on the axes using the provided x and y data points.
    ax.set_xlabel("X-axis Label") # sets the label for the x-axis to "X-axis Label", which helps to identify what the x-axis represents.
    ax.set_ylabel("Y-axis Label") # sets the label for the y-axis to "Y-axis Label", which helps to identify what the y-axis represents.
    ax.set_title("Line Graph") # sets the title of the plot to "Line Graph", providing a descriptive heading for the visualization.
    plt.show() # displays the figure with the plotted line graph, including the x and y axis labels and the title.
```

3.2 Other libraries

Can also use the combination of Pandas and Seaborn for quick and easy data visualization, especially for statistical plots.